

SEQUENCE LISTING

<110> ALBANI, SALVATORE

<120> METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION
AND MODULATION OF ANTIGEN-SPECIFIC T CELLS

<130> AND-TCCCIPI1-DIV2

<140>

<141>

<150> 09/756,983

<151> 2001-01-09

<150> PCT/US99/24666

<151> 1999-10-19

<150> 09/421,506

<151> 1999-10-19

<150> 60/105,018

<151> 1998-10-20

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived
from third hyper V region of IE molecule of Mus musculus

<400> 1

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Phe | Glu | Ala | Gln | Gly | Ala | Leu | Ala | Asn | Ile | Ala | Val | Asp | Lys |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

Ala

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived
from bole I protein of Epstein Barr virus

<400> 2

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Asp | Asp | Ala | Glu | Tyr | Leu | Leu | Gly | Arg | Glu | Ser | Val | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

<210> 3
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide derived
 from the haemophilus influenza virus

<400> 3
 Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys
 1 5 10 15

<210> 4
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide derived
 from the TCR receptor of Mus musculus

<220>
 <221> MOD_RES
 <222> (18)
 <223> Ser, Ile or Thr

<400> 4
 Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys
 1 5 10 15

Ala Xaa Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro
 20 25 30

Gly Thr Arg Leu
 35

<210> 5
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide derived
 from the influenza virus

<400> 5
 Gly Ile Leu Gly Phe Val Phe Thr Leu
 1 5

<210> 6
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived from the influenza virus

<400> 6

Val Lys Leu Gly Glu Phe Tyr Asn Gln
1 5

<210> 7

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (2)

<223> cyclohexylalanine

<400> 7

Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala
1 5 10

<210> 8

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived from the influenza virus

<400> 8

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

<210> 9

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial

<400> 9

Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
1 5 10 15

Arg

<210> 10
 <211> 15
 <212> PRT
 <213> Escherichia coli

<400> 10
 Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu
 1 5 10 15

<210> 11
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 11
 Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly
 1 5 10 15

<210> 12
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 12
 Gly Ile Leu Gly Phe Val Phe Thr Leu
 1 5

<210> 13
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 13
 Val Lys Leu Gly Glu Phe Tyr Asn Gln
 1 5

<210> 14
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 14
 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
 1 5 10

<210> 15
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct with
 human and bacterial sequences

<220>

<221> CDS

<222> (1)..(939)

<400> 15

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|---|-----|
| atg ggc cac aca cgg agg cag gga aca tca cca tcc aag tgt cca tac | 48 |
| Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr | |
| 1 5 10 15 | |
| ctc aat ttc ttt cag ctc ttg gtg ctg gct ggt ctt tct cac ttc tgt | 96 |
| Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys | |
| 20 25 30 | |
| tca ggt gtt atc cac gtg acc aag gaa gtg aaa gaa gtg gca acg ctg | 144 |
| Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu | |
| 35 40 45 | |
| tcc tgt ggt cac aat gtt tct gtt gaa gag ctg gca caa act cgc atc | 192 |
| Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile | |
| 50 55 60 | |
| tac tgg caa aag gag aag aaa atg gtg ctg act atg atg tct ggg gac | 240 |
| Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp | |
| 65 70 75 80 | |
| atg aat ata tgg ccc gag tac aag aac cgg acc atc ttt gat atc act | 288 |
| Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr | |
| 85 90 95 | |
| aat aac ctc tcc att gtg atc ctg gct ctg cgc cca tct gac gag ggc | 336 |
| Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly | |
| 100 105 110 | |
| aca tac gag tgt gtt gtt ctg aag tat gaa aaa gac gct ttc aag cgg | 384 |
| Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg | |
| 115 120 125 | |
| gaa cac ctg gct gaa gtg acg tta tca gtc aaa gct gac ttc cct aca | 432 |
| Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr | |
| 130 135 140 | |
| cct agt ata tct gac ttt gaa att cca act tct aat att aga agg ata | 480 |
| Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile | |
| 145 150 155 160 | |
| att tgc tca acc tct gga ggt ttt cca gag cct cac ctc tcc tgg ttg | 528 |
| Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu | |
| 165 170 175 | |
| gaa aat gga gaa gaa tta aat gcc atc aac aca aca gtt tcc caa gat | 576 |
| Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp | |
| 180 185 190 | |
| cct gaa act gag ctc tat gct gtt agc gaa ttc ggc ggc tcc ggt ggt | 624 |
| Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly | |
| 195 200 205 | |

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agc gcc aca cct caa aat att act gat ttg tgt gca gaa tac cac aac 672
Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn
    210                      215                      220

aca caa ata cat acg cta aat gat aag ata ttt tcg tat aca gaa tct 720
Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser
    225                      230                      235                      240

cta gct gga aaa aga gag atg gct atc att act ttt aag aat ggt gca 768
Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala
    245                      250                      255

act ttt caa gta gaa gta cca ggt agt caa cat ata gat tca caa aaa 816
Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys
    260                      265                      270

aaa gcg att gaa agg atg aag gat acc ctg agg att gca tat ctt act 864
Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr
    275                      280                      285

gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa acg cct cat 912
Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His
    290                      295                      300

gcg att gcc gca att agt atg gca aat taa 942
Ala Ile Ala Ala Ile Ser Met Ala Asn
    305                      310

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<210> 16

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 16

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Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
  1                      5                      10                      15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
    20                      25                      30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
    35                      40                      45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
    50                      55                      60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
    65                      70                      75                      80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
    85                      90                      95

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Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
    100                                105                    110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
    115                                120                    125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
    130                                135                    140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
    145                                150                    155                    160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
    165                                170                    175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
    180                                185                    190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly
    195                                200                    205

Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn
    210                                215                    220

Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser
    225                                230                    235                    240

Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala
    245                                250                    255

Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys
    260                                265                    270

Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr
    275                                280                    285

Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His
    290                                295                    300

Ala Ile Ala Ala Ile Ser Met Ala Asn
    305                                310

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<210> 17

<211> 1056

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<220>

<221> CDS

<222> (1)..(1053)

<400> 17

| | |
|---|-----|
| atg gga ctg agt aac att ctc ttt gtg atg gcc ttc ctg ctc tct ggt | 48 |
| Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly | |
| 1 5 10 15 | |
| gct gct cct ctg aag att caa gct tat ttc aat gag act gca gac ctg | 96 |
| Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu | |
| 20 25 30 | |
| cca tgc caa ttt gca aac tct caa aac caa agc ctg agt gag cta gta | 144 |
| Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val | |
| 35 40 45 | |
| gta ttt tgg cag gac cag gaa aac ttg gtt ctg aat gag gta tac tta | 192 |
| Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu | |
| 50 55 60 | |
| ggc aaa gag aaa ttt gac agt gtt cat tcc aag tat atg ggc cgc aca | 240 |
| Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr | |
| 65 70 75 80 | |
| agt ttt gat tcg gac agt tgg acc ctg aga ctt cac aat ctt cag atc | 288 |
| Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile | |
| 85 90 95 | |
| aag gac aag ggc ttg tat caa tgt atc atc cat cac aaa aag ccc aca | 336 |
| Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr | |
| 100 105 110 | |
| gga atg att cgc atc cac cag atg aat tct gaa ctg tca gtg ctt gct | 384 |
| Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala | |
| 115 120 125 | |
| aac ttc agt caa cct gaa ata gta cca att tct aat ata aca gaa aat | 432 |
| Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn | |
| 130 135 140 | |
| gtg tac ata aat ttg acc tgc tca tct ata cac ggt tac cca gaa cct | 480 |
| Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro | |
| 145 150 155 160 | |
| aag aag atg agt gtt ttg cta aga acc aag aat tca act atc gag tat | 528 |
| Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr | |
| 165 170 175 | |
| gat ggt att atg cag aaa tct caa gat aat gtc aca gaa ctg tac gac | 576 |
| Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp | |
| 180 185 190 | |
| gtt tcc atc agc ttg tct gtt tca ttc cct gat gtt acg agc aat atg | 624 |
| Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met | |
| 195 200 205 | |
| acc atc ttc tgt att ctg gaa act gac aag acg cgg ctt tta tct tca | 672 |
| Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser | |
| 210 215 220 | |


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cct ttc tct ata gag ctt gag gac cct cag cct ccc cca gac cac gaa 720
Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu
225                230                235                240

ttc ggc ggc tcc ggt ggt agc gcc aca cct caa aat att act gat ttg 768
Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu
                245                250                255

tgt gca gaa tac cac aac aca caa ata cat acg cta aat gat aag ata 816
Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile
                260                265                270

ttt tcg tat aca gaa tct cta gct gga aaa aga gag atg gct atc att 864
Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile
                275                280                285

act ttt aag aat ggt gca act ttt caa gta gaa gta cca ggt agt caa 912
Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln
                290                295                300

cat ata gat tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg 960
His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu
305                310                315                320

agg att gca tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg 1008
Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp
                325                330                335

aat aat aaa acg cct cat gcg att gcc gca att agt atg gca aat taa 1056
Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
                340                345                350

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<210> 18

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 18

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Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
 1                5                10                15

Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
                20                25                30

Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
                35                40                45

Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
 50                55                60

Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
65                70                75                80

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Phe | Asp | Ser | Asp | Ser | Trp | Thr | Leu | Arg | Leu | His | Asn | Leu | Gln | Ile | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Lys | Asp | Lys | Gly | Leu | Tyr | Gln | Cys | Ile | Ile | His | His | Lys | Lys | Pro | Thr | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Gly | Met | Ile | Arg | Ile | His | Gln | Met | Asn | Ser | Glu | Leu | Ser | Val | Leu | Ala | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Asn | Phe | Ser | Gln | Pro | Glu | Ile | Val | Pro | Ile | Ser | Asn | Ile | Thr | Glu | Asn | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| Val | Tyr | Ile | Asn | Leu | Thr | Cys | Ser | Ser | Ile | His | Gly | Tyr | Pro | Glu | Pro | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Lys | Lys | Met | Ser | Val | Leu | Leu | Arg | Thr | Lys | Asn | Ser | Thr | Ile | Glu | Tyr | |
| | | | 165 | | | | | | 170 | | | | | 175 | | |
| Asp | Gly | Ile | Met | Gln | Lys | Ser | Gln | Asp | Asn | Val | Thr | Glu | Leu | Tyr | Asp | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Val | Ser | Ile | Ser | Leu | Ser | Val | Ser | Phe | Pro | Asp | Val | Thr | Ser | Asn | Met | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Thr | Ile | Phe | Cys | Ile | Leu | Glu | Thr | Asp | Lys | Thr | Arg | Leu | Leu | Ser | Ser | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Pro | Phe | Ser | Ile | Glu | Leu | Glu | Asp | Pro | Gln | Pro | Pro | Pro | Asp | His | Glu | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Phe | Gly | Gly | Ser | Gly | Gly | Ser | Ala | Thr | Pro | Gln | Asn | Ile | Thr | Asp | Leu | |
| | | | 245 | | | | | | 250 | | | | | 255 | | |
| Cys | Ala | Glu | Tyr | His | Asn | Thr | Gln | Ile | His | Thr | Leu | Asn | Asp | Lys | Ile | |
| | | 260 | | | | | 265 | | | | | | 270 | | | |
| Phe | Ser | Tyr | Thr | Glu | Ser | Leu | Ala | Gly | Lys | Arg | Glu | Met | Ala | Ile | Ile | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Thr | Phe | Lys | Asn | Gly | Ala | Thr | Phe | Gln | Val | Glu | Val | Pro | Gly | Ser | Gln | |
| | | 290 | | | | 295 | | | | | 300 | | | | | |
| His | Ile | Asp | Ser | Gln | Lys | Lys | Ala | Ile | Glu | Arg | Met | Lys | Asp | Thr | Leu | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Arg | Ile | Ala | Tyr | Leu | Thr | Glu | Ala | Lys | Val | Glu | Lys | Leu | Cys | Val | Trp | |
| | | | 325 | | | | | | 330 | | | | | 335 | | |
| Asn | Asn | Lys | Thr | Pro | His | Ala | Ile | Ala | Ala | Ile | Ser | Met | Ala | Asn | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |

<210> 19

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 19

Ser Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala
 1 5 10 15

Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln
 20 25 30

<210> 20

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 20

Ala Gln Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln
 1 5 10 15

Leu Lys Gln Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln
 20 25 30

<210> 21

<211> 1095

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<220>

<221> CDS

<222> (1)..(1092)

<400> 21

atg gcc ata agt gga gtc cct gtg cta gga ttt ttc atc ata gct gtg 48
 Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
 1 5 10 15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc 96
 Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
 20 25 30

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg 144
 Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag 192
 Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60

| | | | | | | | | | | | | | | | | |
|------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| gag Glu 65 | acg Thr | gtc Val | tgg Trp | cgg Arg | ctt Leu | gaa Glu | gaa Glu | ttt Phe | gga Gly | cga Arg | ttt Phe | gcc Ala | agc Ser | ttt Phe | gag Glu | 240 |
| gct Ala | caa Gln | ggt Gly | gca Ala | ttg Leu | gcc Ala | aac Asn | ata Ile | gct Ala | gtg Val | gac Asp | aaa Lys | gcc Ala | aac Asn | ctg Leu | gaa Glu | 288 |
| atc Ile | atg Met | aca Thr | aag Lys | cgc Arg | tcc Ser | aac Asn | tat Tyr | act Thr | ccg Pro | atc Ile | acc Thr | aat Asn | gta Val | cct Pro | cca Pro | 336 |
| gag Glu | gta Val | act Thr | gtg Val | ctc Leu | acg Thr | aac Asn | agc Ser | cct Pro | gtg Val | gaa Glu | ctg Leu | aga Arg | gag Glu | ccc Pro | aac Asn | 384 |
| gtc Val | ctc Leu | atc Ile | tgt Cys | ttc Phe | atc Ile | gac Asp | aag Lys | ttc Phe | acc Thr | cca Pro | cca Pro | gtg Val | gtc Val | aat Asn | gtc Val | 432 |
| acg Thr | tgg Trp | ctt Leu | cga Arg | aat Asn | gga Gly | aaa Lys | cct Pro | gtc Val | acc Thr | aca Thr | gga Gly | gtg Val | tca Ser | gag Glu | aca Thr | 480 |
| gtc Val | ttc Phe | ctg Leu | ccc Pro | agg Arg | gaa Glu | gac Asp | cac His | ctt Leu | ttc Phe | cgc Arg | aag Lys | ttc Phe | cac His | tat Tyr | ctc Leu | 528 |
| ccc Pro | ttc Phe | ctg Leu | ccc Pro | tca Ser | act Thr | gag Glu | gac Asp | gtt Val | tac Tyr | gac Asp | tgc Cys | agg Arg | gtg Val | gag Glu | cac His | 576 |
| tgg Trp | ggc Gly | ttg Leu | gat Asp | gag Glu | cct Pro | ctt Leu | ctc Leu | aag Lys | cac His | tgg Trp | gag Glu | ttt Phe | gat Asp | gct Ala | cca Pro | 624 |
| agc Ser | cct Pro | ctc Leu | cca Pro | gag Glu | act Thr | aca Thr | gag Glu | gaa Glu | ttc Phe | ggc Gly | ggc Gly | tcc Ser | ggc Gly | ggc Gly | tcc Ser | 672 |
| gcg Ala | cag Gln | ctg Leu | gaa Glu | tgg Trp | gaa Glu | ctg Leu | cag Gln | gcg Ala | ctg Leu | gaa Glu | aaa Lys | gaa Glu | aac Asn | gcg Ala | cag Gln | 720 |
| ctg Leu | gaa Glu | tgg Trp | gaa Glu | ctg Leu | cag Gln | gcg Ala | ctg Leu | gaa Glu | aaa Lys | gaa Glu | ctg Leu | gcg Ala | cag Gln | ggc Gly | ggc Gly | 768 |
| tcc Ser | ggc Gly | ggc Gly | agc Ser | gcc Ala | aca Thr | cct Pro | caa Gln | aat Asn | att Ile | act Thr | gat Asp | ttg Leu | tgt Cys | gca Ala | gaa Glu | 816 |
| tac Tyr | cac His | aac Asn | aca Thr | caa Gln | ata Ile | cat His | acg Thr | cta Leu | aat Asn | gat Asp | aag Lys | ata Ile | ttt Phe | tcg Ser | tat Tyr | 864 |

aca gaa tct cta gct gga aaa aga gag atg gct atc att act ttt aag 912
 Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
 290 295 300
 aat ggt gca act ttt caa gta gaa gta cca ggt agt caa cat ata gat 960
 Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
 305 310 315 320
 tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg agg att gca 1008
 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
 325 330 335
 tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa 1056
 Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
 340 345 350
 acg cct cat gcg att gcc gca att agt atg gca aat taa 1095
 Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 355 360

<210> 22

<211> 364

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 22

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
 1 5 10 15
 Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
 20 25 30
 Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45
 Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60
 Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65 70 75 80
 Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
 85 90 95
 Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110
 Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125
 Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
 130 135 140

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Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145                      150                      155                      160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
                      165                      170                      175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
                      180                      185                      190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
195                      200                      205

Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser
210                      215                      220

Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln
225                      230                      235                      240

Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly
245                      250                      255

Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu
260                      265                      270

Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr
275                      280                      285

Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
290                      295                      300

Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
305                      310                      315                      320

Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
325                      330                      335

Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
340                      345                      350

Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
355                      360

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<210> 23

<211> 861

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<220>

<221> CDS

<222> (1)..(855)

<400> 23

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | gtg | tgt | ctg | aag | ttc | cct | gga | ggc | tcc | tgc | atg | gca | gct | ctg | aca | 48 |
| Met | Val | Cys | Leu | Lys | Phe | Pro | Gly | Gly | Ser | Cys | Met | Ala | Ala | Leu | Thr | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| gtg | aca | ctg | atg | gtg | ctg | agc | tcc | cca | ctg | gct | ttg | gct | ggg | gac | acc | 96 |
| Val | Thr | Leu | Met | Val | Leu | Ser | Ser | Pro | Leu | Ala | Leu | Ala | Gly | Asp | Thr | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| cga | cca | cgt | ttc | ttg | gag | cag | gtt | aaa | cat | gag | tgt | cat | ttc | ttc | aac | 144 |
| Arg | Pro | Arg | Phe | Leu | Glu | Gln | Val | Lys | His | Glu | Cys | His | Phe | Phe | Asn | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| ggg | acg | gag | cgg | gtg | cgg | ttc | ctg | gac | aga | tac | ttc | tat | cac | caa | gag | 192 |
| Gly | Thr | Glu | Arg | Val | Arg | Phe | Leu | Asp | Arg | Tyr | Phe | Tyr | His | Gln | Glu | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| gag | tac | gtg | cgc | ttc | gac | agc | gac | gtg | ggg | gag | tac | cgg | gcg | gtg | acg | 240 |
| Glu | Tyr | Val | Arg | Phe | Asp | Ser | Asp | Val | Gly | Glu | Tyr | Arg | Ala | Val | Thr | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | |
| gag | ctg | ggg | cgg | cct | gat | gcc | gag | tac | tgg | aac | agc | cag | aag | gac | ctc | 288 |
| Glu | Leu | Gly | Arg | Pro | Asp | Ala | Glu | Tyr | Trp | Asn | Ser | Gln | Lys | Asp | Leu | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| ctg | gag | cag | aag | cgg | gcc | gcg | gtg | gac | acc | tac | tgc | aga | cac | aac | tac | 336 |
| Leu | Glu | Gln | Lys | Arg | Ala | Ala | Val | Asp | Thr | Tyr | Cys | Arg | His | Asn | Tyr | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| ggg | gtt | ggt | gag | agc | ttc | aca | gtg | cag | cgg | cga | gtc | tat | cct | gag | gtg | 384 |
| Gly | Val | Gly | Glu | Ser | Phe | Thr | Val | Gln | Arg | Arg | Val | Tyr | Pro | Glu | Val | |
| | 115 | | | | | | 120 | | | | | 125 | | | | |
| act | gtg | tat | cct | gca | aag | acc | cag | ccc | ctg | cag | cac | cac | aac | ctc | ctg | 432 |
| Thr | Val | Tyr | Pro | Ala | Lys | Thr | Gln | Pro | Leu | Gln | His | His | Asn | Leu | Leu | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| gtc | tgc | tct | gtg | aat | ggt | ttc | tat | cca | ggc | agc | att | gaa | gtc | agg | tgg | 480 |
| Val | Cys | Ser | Val | Asn | Gly | Phe | Tyr | Pro | Gly | Ser | Ile | Glu | Val | Arg | Trp | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| ttc | cgg | aac | ggc | cag | gaa | gag | aag | act | ggg | gtg | gtg | tcc | aca | ggc | ctg | 528 |
| Phe | Arg | Asn | Gly | Gln | Glu | Glu | Lys | Thr | Gly | Val | Val | Ser | Thr | Gly | Leu | |
| | | | 165 | | | | | | 170 | | | | | 175 | | |
| atc | cag | aat | gga | gac | tgg | acc | ttc | cag | acc | ctg | gtg | atg | ctg | gaa | aca | 576 |
| Ile | Gln | Asn | Gly | Asp | Trp | Thr | Phe | Gln | Thr | Leu | Val | Met | Leu | Glu | Thr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| gtt | cct | cgg | agt | gga | gag | gtt | tac | acc | tgc | caa | gtg | gag | cac | cca | agc | 624 |
| Val | Pro | Arg | Ser | Gly | Glu | Val | Tyr | Thr | Cys | Gln | Val | Glu | His | Pro | Ser | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| ctg | acg | agc | cct | ctc | aca | gtg | gaa | tgg | aga | gca | cgg | tct | gaa | tct | gca | 672 |
| Leu | Thr | Ser | Pro | Leu | Thr | Val | Glu | Trp | Arg | Ala | Arg | Ser | Glu | Ser | Ala | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |

cag agc aag ggc ggc tcc ggt ggt agc gcc cag ctg aag aag aaa ctc 720
 Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu
 225 230 235 240

cag gct ctg aaa aaa aag aat gcc cag ctc aag cag aag ctg cag gcc 768
 Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala
 245 250 255

ctg aag aaa aag ctg gct cag ggt tcc ggt ggt tcc gcg ggt ggt ggt 816
 Leu Lys Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly
 260 265 270

ttg aac gac atc ttc gaa gct cag aaa atc gaa tgg cac taataa 861
 Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
 275 280 285

<210> 24

<211> 285

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 24

Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr
 1 5 10 15

Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr
 20 25 30

Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn
 35 40 45

Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu
 50 55 60

Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
 65 70 75 80

Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
 85 90 95

Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr
 100 105 110

Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val
 115 120 125

Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
 130 135 140

Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
 145 150 155 160

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Arg | Asn | Gly | Gln | Glu | Glu | Lys | Thr | Gly | Val | Val | Ser | Thr | Gly | Leu |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Ile | Gln | Asn | Gly | Asp | Trp | Thr | Phe | Gln | Thr | Leu | Val | Met | Leu | Glu | Thr |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Val | Pro | Arg | Ser | Gly | Glu | Val | Tyr | Thr | Cys | Gln | Val | Glu | His | Pro | Ser |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Leu | Thr | Ser | Pro | Leu | Thr | Val | Glu | Trp | Arg | Ala | Arg | Ser | Glu | Ser | Ala |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Gln | Ser | Lys | Gly | Gly | Ser | Gly | Gly | Ser | Ala | Gln | Leu | Lys | Lys | Lys | Leu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Gln | Ala | Leu | Lys | Lys | Lys | Asn | Ala | Gln | Leu | Lys | Gln | Lys | Leu | Gln | Ala |
| | | | 245 | | | | | 250 | | | | | | 255 | |
| Leu | Lys | Lys | Lys | Leu | Ala | Gln | Gly | Ser | Gly | Gly | Ser | Ala | Gly | Gly | Gly |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Leu | Asn | Asp | Ile | Phe | Glu | Ala | Gln | Lys | Ile | Glu | Trp | His | | | |
| | 275 | | | | | | 280 | | | | | 285 | | | |